Amendments to the Specification:

Please replace paragraph [0001] with the following amended paragraph:

[0001] This application claims the benefit of U.S. application Serial No. 60/271,703 filed February 27, 2001, the disclosure of which is incorporated herein by reference.

Please replace paragraphs [0018] with the following rewritten paragraph:

[0018] Figure 3c shows DNA sequencing on pooled genomic DNA, over SNP 466F, the sequence of the nucleic acid should be [C/T/G]AAGGTTGTCCT (SEQ. ID NO: 1) 40µl PCR product was incubated with 15µl magnetic beads (10µg/µl) and 25µl 2 x BW buffer. Pyrosequencing™ was then performed on a PSQ™ 96 system instrument using Pyrosequencing™ SNP reagent kit. The peak heights were measured in order to calculate the frequency of the allele. The results are shown generally as nucleotide incorporated (i.e. A, C, G or T) versus amount of light released (in RLU). The 3 nucleotide incorporations which relate to the SNP are marked. The experimental conditions are as described in Example 4.

Please replace paragraph [0019] with the following rewritten paragraph:

[0019] Figure 3d shows DNA sequencing on pooled genomic DNA, over SNP 465R, the sequence of the nucleic acid should be [C/T] GTTCCACCT (SEQ. ID NO: 2). 40µl PCR product was incubated with 15µl magnetic beads (10µg/µl) and 25µl 2 x BW buffer. Pyrosequencing™ was then performed on a PSQ™ 96 system instrument using Pyrosequencing™ SNP reagent kit. The peak heights were measured in order to calculate the

frequency of the allele. The results are shown generally as nucleotide incorporated (i.e. A, C, G or T) versus amount of light released (in RLU). The 2 nucleotide incorporations which relate to the SNP are marked. The experimental conditions are as described in Example 4.

Please replace paragraph [00130] with the following rewritten paragraph:

[00130] PCR amplification primers and sequencing primers were designed using Oligo 6.0 (Med Probe AS, Oslo, Norway). All primers were ordered from Interactiva (Supra).

SNP_ID	Upstream primer	Downstream primer	Sequencing primer	Fragment length [bp]	Sequencing output
Eu1 (ACP-240)	E1a (SEQ ID NO: 3) 5'-Biotin-ggt cgg gct ggg aag at-3'	E1b (SEQ ID NO: 4) 5'-gct ccc gca gag gaa gc-3'	E1s (SEQ ID NO: 5) 5'-aga aag ggc ctc ctc tct tt-3'	158	A/T
Eu4 (ACEex 15)	E4a (SEQ ID NO: 6) 5'-gcc agg aag ttt gat gtg aac-3'	E4b (SEQ ID NO: 7) 5'-Biotin-gat tcc cct ctc cct gta cct-3'	E4s (SEQ ID NO: 8 5'-gac cta gaa cgg gca gc 3'	145	A/G
Eu7 (ANP1218)	E7a (SEQ ID NO: 9) 5'-Biotin-tga tgt aac cct cct ctc ca 3'	E7b (SEQ ID NO: 10) 5'-cgg ctt acc ttc tgc tgt agt-3'	E7s (SEQ ID NO: 11) 5'-acg gca gct tct tcc cc-3'	142	C/T
460R	PSO 145 (SEQ ID NO: 12) 5'-B-ggc tgc tgt tct gaa acc atc tga -3'	PSO 146 (SEQ ID NO: 13) 5' -ttc agg aac gcg ggc aag tc -3'	PSO 147 (SEQ ID NO: 14) 5' -gag cag tcc cca ccc -3'	101	CC/T
461R	Same as 460R	Same as 460R	PSO 148 (SEQ ID NO: 15) 5' -gcg ggc aag tcc aat -3'	Same as 460R	C/TT
465R	PSO 149 (SEQ ID	PSO 150 (SEQ ID NO:	PSO 151 (SEQ ID NO: 18)	85	C/T

SNP_ID	Upstream primer	Downstream primer	Sequencing primer	Fragment length [bp]	Sequencing output
	NO: 16) 5' -B-gga aca ctg cct ccc act ttc tt -3'	17) 5' -tcc cca tgc agc cct aga gac -3'	5' -gga gaa gtc cag tgt gc -3'		
466F	PSO 182 (SEQ ID NO: 19) 5' -ttc caa agg acg cga cca taa -3'	PSO 183 (SEQ ID NO: 20) 5' -B-cct gca ccc cag acc act ga -3'	PSO 184 (SEQ ID NO: 21) 5' -tag ctg cgc ggg aa -3'	111	C/T/G
470R	PSO 155 (SEQ ID NO: 22) 5' -B-cct acc cac agg cca gaa -3'	PSO 156 (SEQ ID NO: 23) 5' -gcc tgg gac ctc act gtc -3'	PSO 157 (SEQ ID NO: 24) 5' -gga gac aga atg ctg at -3'	102	C/A
471F	PSO 158 (SEQ ID NO: 25) 5' -gtt gcc ctc tgg ttc cac ct -3'	PSO 159 (SEQ ID NO: 26) 5' -B-tgt ctc cag cag ctc ctt cat c -3'	PSO 160 (SEQ ID NO: 27) 5' -gcc cag gaa gga ac -3'	126	CCC/T
481R	PSO 167 (SEQ ID NO: 28) 5' -B-gat gct gta aca gag acc cca ta -3'	PSO 168 (SEQ ID NO: 29) 5' -ctg gga tta cag gtg tga aca ct -3'	PSO 169 (SEQ ID NO: 30) 5' -tag gag caa gaa gta aac -3'	110	T/G
486R	PSO 173 (SEQ ID NO: 31) 5' -B-caa ggt aga gaa gtg cag cat tca -3'	PSO 174 (SEQ ID NO: 32) 5' -ttg att ctc ttt gag ccc aga tgt -3'	PSO 175 (SEQ ID NO: 33) 5' -gcc tgg agc tgt taa t -3'	115	TT/C
1000F	PSO 194	PSO 195	PSO 196	159	CC/T
3345F	PSO 199	PSO 200	PSO 201	120	A/GGGG

Table 1: Primers and SNP definitions

SNP name	Oligoname	Oligo Sequence	Sequencing output
Oligo 1	PSO43SNP	AGTCATGGTGCTGGGGCACTGGCC **GTCGTTTTACAACG** (SEQ ID NO: 34)	CCCC/T
	PSO44SNP	AGTCATGGTGCTAGGGCACTGGCC **GTCGTTTTACAACG** (SEQ ID NO: 35)	
Oligo 2	PSO44SNP	AGTCATGGTGCTGGGGGCACTGGC **CGTCGTTTTACAACG** (SEQ ID NO: 36)	CCCCC/T
	PSO45SNP	AGTCATGGTGCTAGGGGCACTGGC **CGTCGTTTTACAACG** (SEQ ID NO: 37)	
Oligo 3	PSO53SNP	AGTCATGGTGCTAAGGGGGCACTG **GCCGTCGTTTTACAACG** (SEQ ID NO: 38)	CCCCC/TTT
	PSO54SNP	AGTCATGGTGCTAAAGGGGCACTG **GCCGTCGTTTTACAACG** (SEQ ID NO: 39)	
Sequencing primer	PSO55NUSPT	CGT TGT AAA ACG ACG GC (SEQ ID NO: 40)	

Table 2: Oligonucleotides used to create "artificial" SNPs.

Please replace paragraph [00133] with the following rewritten paragraph:

[00133] In order to calibrate the amount of DNA in each of the samples, an SNP was chosen for analysis. SNP 465R was chosen, it is a C/T SNP that generates good signals without preferential amplification, is not present in a homopolymeric stretch and gives no background signals or uneven peak heights. All samples were genotyped for the chosen SNP.

SNP ID	Upstream primer	Downstream primer	Sequencing primer	Fragment length	SNP	Sequencing output
465R	5 -B-gga aca ctg cct ccc act ttc tt -3' (SEQ ID NO: 16)	5 -tcc cca tgc agc cct aga gac -3 (SEQ ID NO: 17)	5 -gga gaa gtc cag tgt gc -3 (SEQ ID NO: 18)	85	G/A	C/T

Table 3: Primers used to amplify and sequence SNP 465R.

Please replace paragraph [00151] with the following rewritten paragraph:

[00151] Results on allele frequencies were calculated for five different SNPs, the results for which are tabulated below:

SNP	Sequence	Expected Frequency	Measured Frequency
466F	[C/T/G]AAGGTTGTCCT (SEQ ID NO: 1)	C 38.1% T 37.5% G 24.4%	C 40.8% T 32.1% G 27.1%
465R	[C/T]GTTCCACCT (SEQ ID NO: 2)	C 64.4% T 35.6%	C 65.1% T 34.9%
461R	[C/T]TGCAGA	C 92.2% T 7.8%	C 96.5% T 3.5%
470R	T[C/A]TCTGG	C 28.9% A 71.1%	C 28.2% C 71.8%
Eu4	[A/G]CTGCCT	G 56.7% A 43.3%	G 56.0% A 44.0%

Table 8: Results from pooling experiments

Please replace paragraphs [00176] and [00177] in the Abstract with the following rewritten paragraph:

[00176] The present invention related to a method of determining the frequency of an allele in a population of nucleic acid molecules[[, said]]. The method [[comprising:]] comprises ~~[00177]~~ pooling the nucleic acid molecules of [[said]] a population of nucleic acids, performing primer extension reactions using a primer which binds at a predetermined site located in [[said]] the nucleic acid molecules, and obtaining a pattern of nucleotide incorporation.

After the Drawings, please insert the attached Sequence Listing.